FIGURE 1

Monkey #6 (Intranodal Administration)

Legend: D0, D68, D82

Y-axis: Spots/1E6 Cells (0, 5, 10, 15, 20, 25)
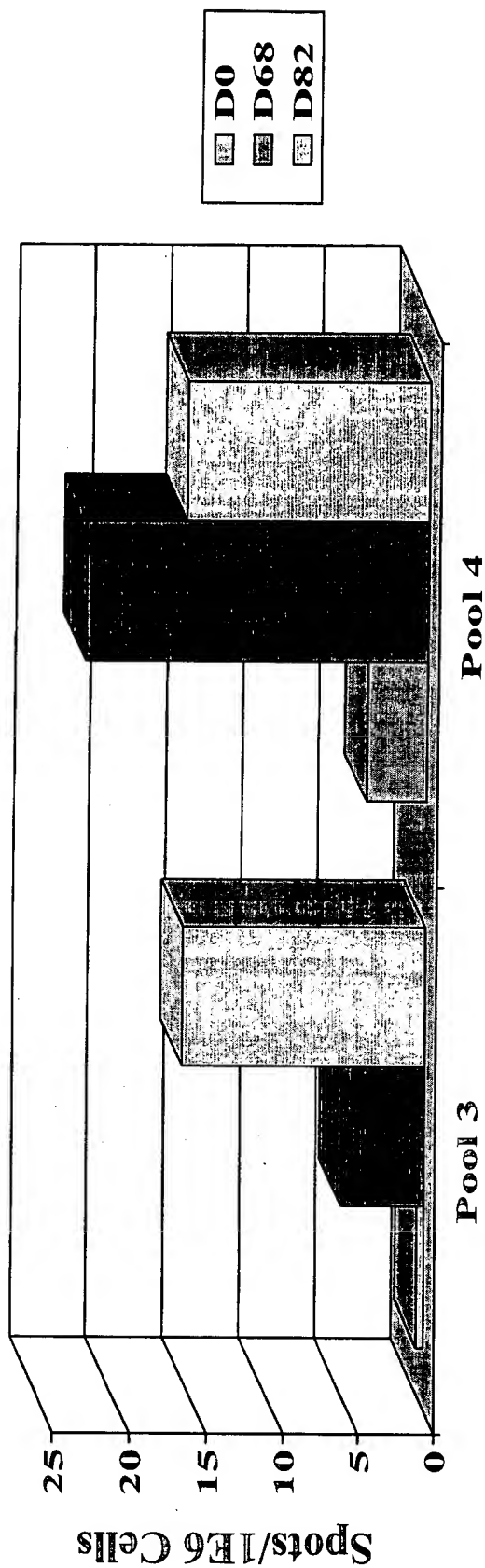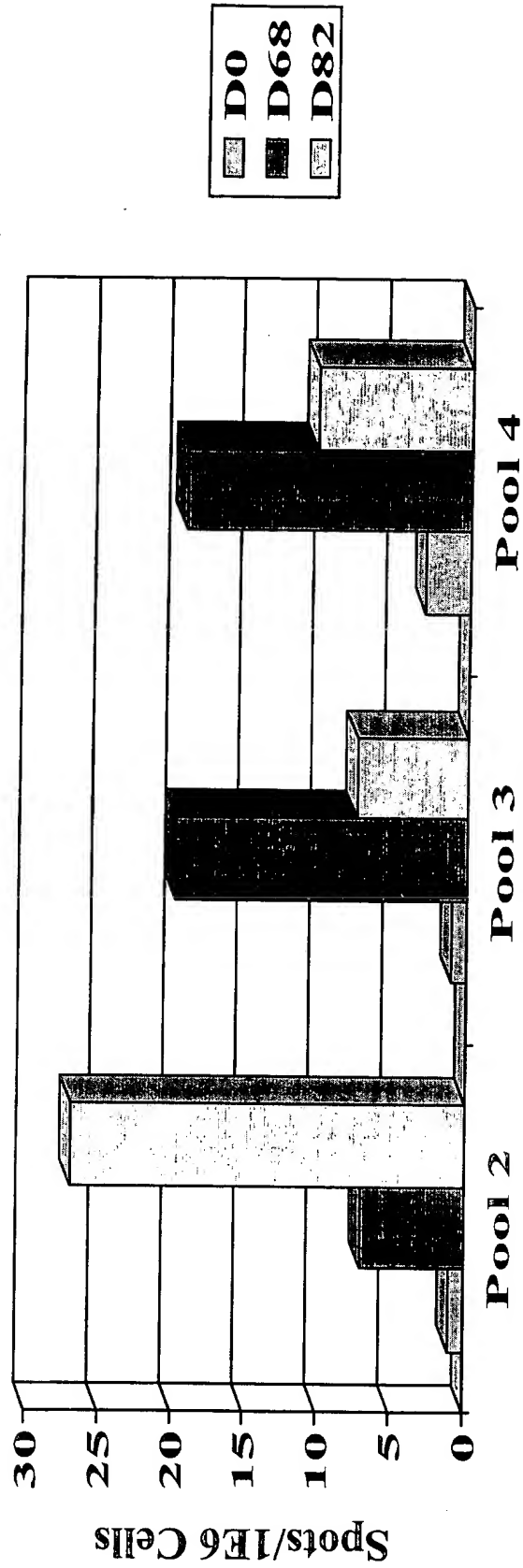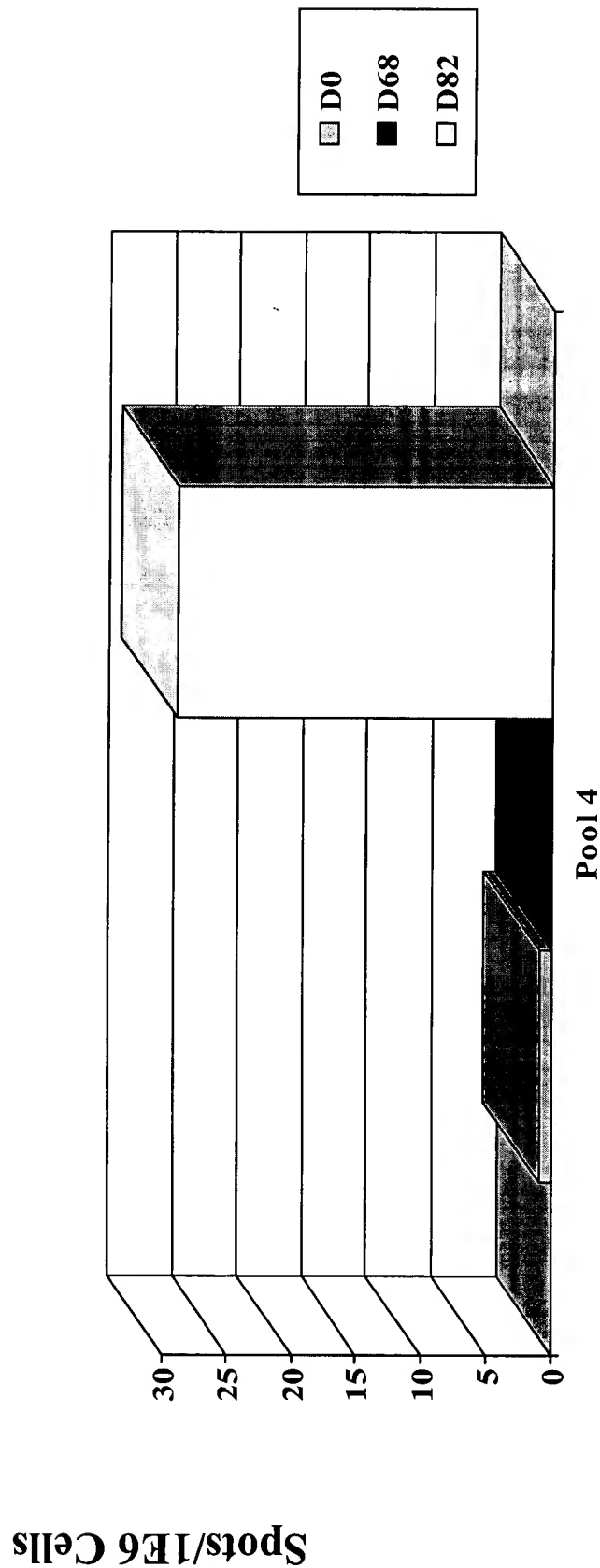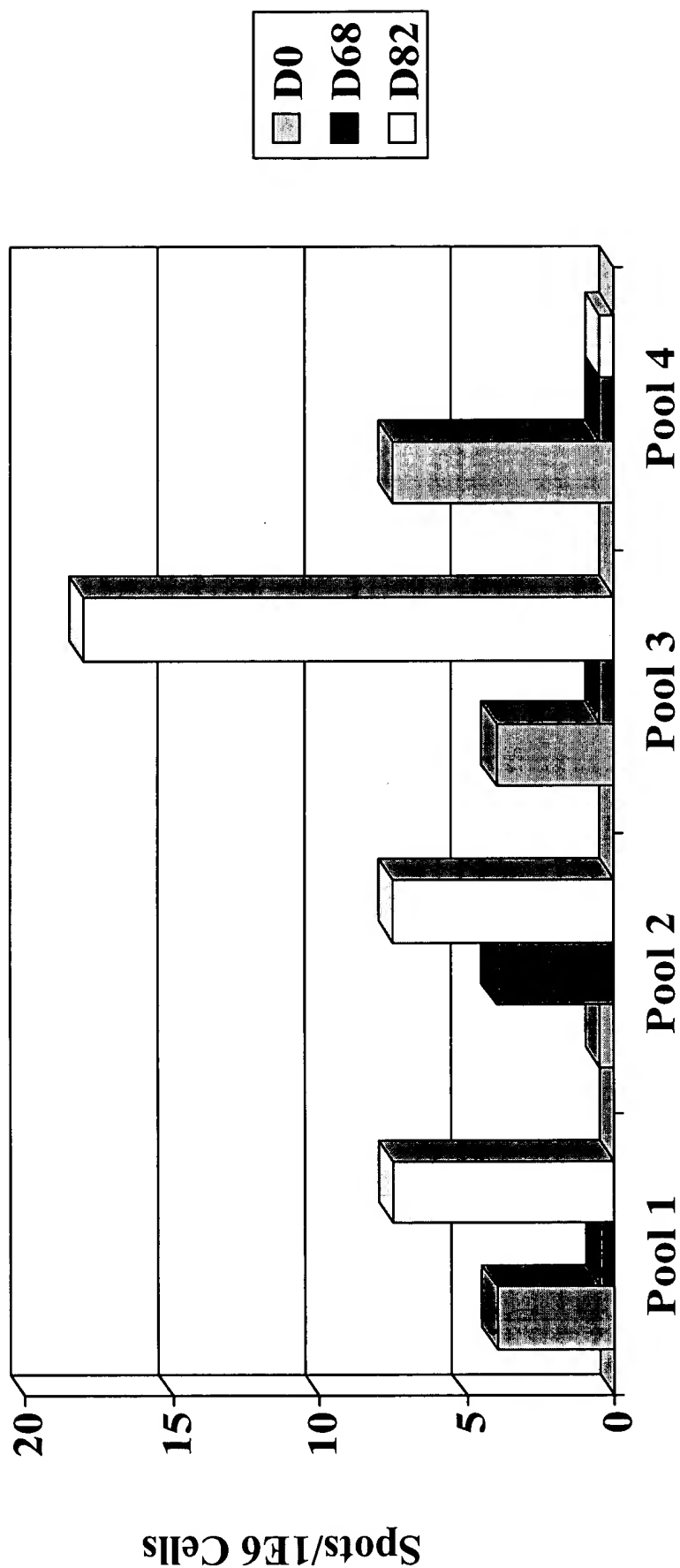
X-axis: Pool 3, Pool 4

FIGURE 2

Monkey #7 (Intranodal Administration)

FIGURE 3

Monkey # 11 (Subcutaneous Administration)

FIGURE 4

Monkey #10 (Subcutaneous Administration)

FIGURE 5

Antibodies to gp100

Kinetics ELISA mOD/min

Day of bleed

CONTROL
subcutaneous
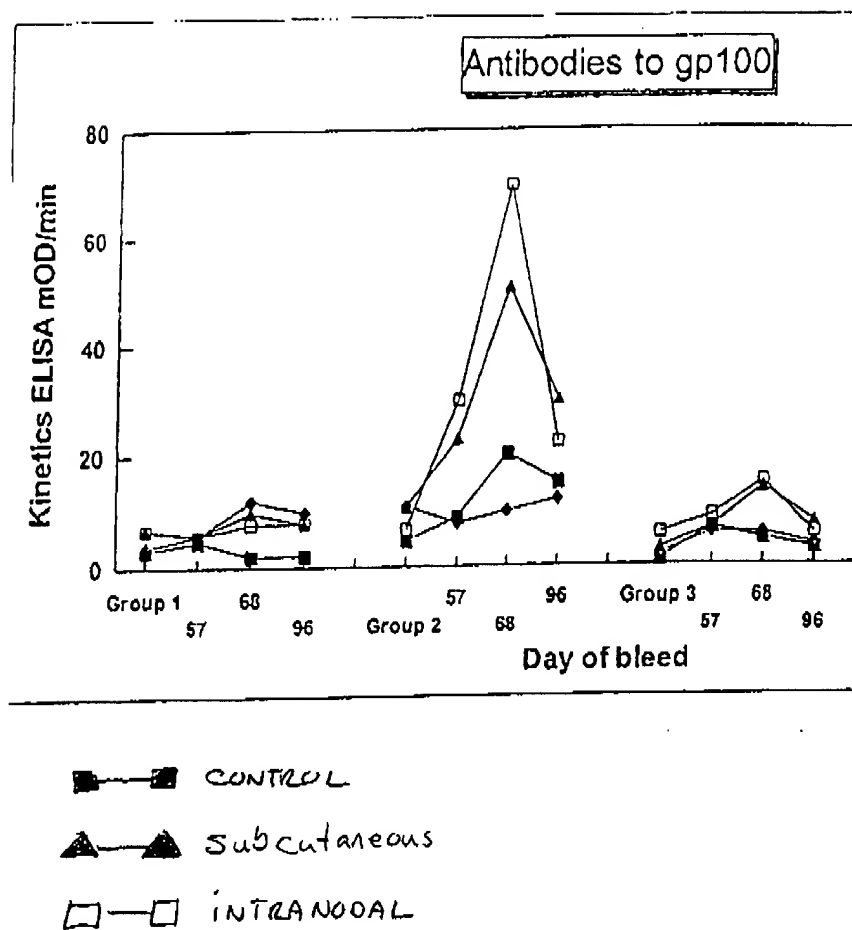INTRANODAL

FIGURE 6

```
                         ATGG ATCTGGTGCT AAAAAGATGC CTTCTTCATT TGGCTGTGAT
AGGTGCTTTG CTGGCTGTGG GGGCTACAAA AGTACCCAGA AACCAGGACT GGCTTGGTGT
CTCAAGGCAA CTCAGAACCA AAGCCTGGAA CAGGCAGCTG TATCCAGAGT GGACAGAAGC
CCAGAGACTT GACTGCTGGA GAGGTGGTCA AGTGTCCCTC AAGGTCAGTA ATGATGGGCC
TACACTGATT GGTGCAAATG CCTCCTTCTC TATTGCCTTG AACTTCCCTG GAAGCCAAAA
GGTATTGCCA GATGGGCAGG TTATCTGGGT CAACAATACC ATCATCAATG GGAGCCAGGT
GTGGGCAGGA CAGCCAGTGT ATCCCCAGGA AACTGACGAT GCCTGCATCT TCCCTGATGG
TGGACCTTGC CCATCTGGCT CTTGGTCTCA GAAGAGAAGC TTTGTTTATG TCTGGAAGAC
CTGGGGCCAA TACTGGCAAG TTCTAGGGGG CCCAGTGTCT GGGCTGAGCA TTGGGACAGG
CAGGGCAATG CTGGGCACAC ACACGATGGA AGTGACTGTC TACCATCGCC GGGGATCCCG
GAGCTATGTG CCTCTTGCTC ATTCCAGCTC AGCCTTCACC ATTATGGACC AGGTGCCTTT
CTCCGTGAGC GTGTCCCAGT TGCGGGCCTT GGATGGAGGG AACAAGCACT TCCTGAGAAA
TCAGCCTCTG ACCTTTGCCC TCCAGCTCCA TGACCCCAGT GGCTATCTGG CTGAAGCTGA
CCTCTCCTAC ACCTGGGACT TTGGAGACAG TAGTGGAACC CTGATCTCTC GGGCACTTGT
GGTCACTCAT ACTTACCTGG AGCCTGGCCC AGTCACTGTT CAGGTGGTCC TGCAGGCTGC
CATTCCTCTC ACCTCCTGTG GCTCCTCCCC AGTTCCAGGC ACCACAGATG GGCACAGGCC
AACTGCAGAG GCCCCTAACA CCACAGCTGG CCAAGTGCCT ACTACAGAAG TTGTGGGTAC
TACACCTGGT CAGGCGCCAA CTGCAGAGCC CTCTGGAACC ACATCTGTGC AGGTGCCAAC
CACTGAAGTC ATAAGCACTG CACCTGTGCA GATGCCAACT GCAGAGAGCA CAGGTATGAC
ACCTGAGAAG GTGCCAGTTT CAGAGGTCAT GGGTACCACA CTGGCAGAGA TGTCAACTCC
AGAGGCTACA GGTATGACAC CTGCAGAGGT ATCAATTGTG GTGCTTTCTG GAACCACAGC
TGCACAGGTA ACAACTACAG AGTGGGTGGA GACCACAGCT AGAGAGCTAC CTATCCCTGA
GCCTGAAGGT CCAGATGCCA GCTCAATCAT GTCTACGGAA AGTATTACAG GTTCCCTGGG
CCCCCTGCTG GATGGTACAG CCACCTTAAG GCTGGTGAAG AGACAAGTCC CCCTGGATTG
TGTTCTGTAT CGATATGGTT CCTTTTCCGT CACCCTGGAC ATTGTCCAGG GTATTGAAAG
TGCCGAGATC CTGCAGGCTG TGCCGTCCGG TGAGGGGGAT GCATTTGAGC TGACTGTGTC
CTGCCAAGGC GGGCTGCCCA AGGAAGCCTG CATGGAGATC TCATCGCCAG GGTGCCAGCC
CCCTGCCCAG CGGCTGTGCC AGCCTGTGCT ACCCAGCCCA GCCTGCCAGC TGGTTCTGCA
CCAGATACTG AAGGGTGGCT CGGGGACATA CTGCCTCAAT GTGTCTCTGG CTGATACCAA
CAGCCTGGCA GTGGTCAGCA CCCAGCTTAT CATGCCTGGT CAAGAAGCAG GCCTTGGGCA
GGTTCCGCTG ATCGTGGGCA TCTTGCTGGT GTTGATGGCT GTGGTCCTTG CATCTCTGAT
ATATAGGCGC AGACTTATGA AGCAAGACTT CTCCGTACCC CAGTTGCCAC ATAGCAGCAG
TCACTGGCTG CGTCTACCCC GCATCTTCTG CTCTTGTCCC ATTGGTGAGA ACAGCCCCCT
CCTCAGTGGG CAGCAGGTCT GA
```

FIGURE 7

Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu Ala Val Ile Gly
1   5   10   15

Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn Gln Asp Trp
          20   25   30

Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu
          35   40   45

Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly
          50   55   60

Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
65   70   75   80

Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val
          85   90   95

Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly
          100   105   110

Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp
          115   120   125

Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser
          130   135   140

Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp
145   150   155   160

Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg
          165   170   175

Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
          180   185   190

Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
          195   200   205

Ile Thr^{Met} Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Arg Ala
          210   215   220

Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe
225   230   235   240

Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu
          245   250   255

Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu Ile Ser Arg
          260   265   270

Ala Leu Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr ^{Val}Ala
          275   280   285

Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
          290   295   300

Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala Glu Ala Pro
305   310   315   320

Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr
          325   330   335

Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr Ser Val Gln
          340   345   350

Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln Met Pro Thr
          355   360   365

FIGURE 7 (CONT'D)

```
Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val
    370             375             380
Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala Thr Gly Met
385             390             395             400
Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr Thr Ala Ala
            405             410             415
Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
        420             425             430
Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile Met Ser Thr Glu
        435             440             445
Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr Ala Thr Leu
    450             455             460
Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
465             470             475             480
Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala
            485             490             495
Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu
            500             505             510
Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
            515             520             525
Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Pro Val
    530             535             540
Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile Leu Lys Gly
545             550             555             560
Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
                565             570             575
Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly Gln Glu Ala Gly
            580             585             590
Leu Gly Gln Val Pro Leu Ile Val Gly Ile Leu Leu Val Leu Met Ala
            595             600             605
Val Val Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp
    610             615             620
Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His Trp Leu Arg Leu
625             630             635             640
Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly Glu Asn Ser Pro Leu Leu
                645             650             655
Ser Gly Gln Gln Val
            660
```

```
                           ●                                ●
        ATGGAGTCTCCCTCGGCCCGCCCCACAGATGGTGCATCCCCTGGCAGAGGCTCCTGCT
      1 ---------+---------+---------+---------+---------+---------+ 60
        TACCTCAGAGGGAGCCGGGGAGGGGTGTCTACCACGTAGGGGACCGTCTCCGAGGACGAG

   a    M   E   S   P   S   A   P   P   H   R   W   C   I   P   W   Q   R   L   L   L   -

        ACAGCCTCACTTCTAACCTTCTGGAACCCGCCCACCACTGCCAAGCTCACTATTGAATCC
     61 ---------+---------+---------+---------+---------+---------+ 120
        TGTCGGAGTGAAGATTGGAAGACCTTGGGCGGGTGGTGACGGTTCGAGTGATAACTTAGG

   a    T   A   S   L   L   T   F   W   N   P   P   T   T   A   K   L   T   I   E   S   -

        ACGCCGTTCAATGTCGCAGAGGGGAAGGAGGTGCTTCTACTTGTCCACAATCTGCCCCAG
    121 ---------+---------+---------+---------+---------+---------+ 180
        TGCGGCAAGTTACAGCGTCTCCCCTTCCTCCACGAAGATGAACAGGTGTTAGACGGGGTC

   a    T   P   F   N   V   A   E   G   K   E   V   L   L   L   V   H   N   L   P   Q   -

        CATCTTTTTGGCTACAGCTGGTACAAAGGTGAAAGAGTGGATGGCAACCGTCAAATTATA
    181 ---------+---------+---------+---------+---------+---------+ 240
        GTAGAAAAACCGATGTCGACCATGTTTCCACTTTCTCACCTACCGTTGGCAGTTTAATAT

   a    H   L   F   G   Y   S   W   Y   K   G   E   R   V   D   G   N   R   Q   I   I   -

        GGATATGTAATAGGAACTCAACAAGCTACCCCAGGGCCCGCATACAGTGGTCGAGAGATA
    241 ---------+---------+---------+---------+---------+---------+ 300
        CCTATACATTATCCTTGAGTTGTTCGATGGGGTCCCGGGCGTATGTCACCAGCTCTCTAT

   a    G   Y   V   I   G   T   Q   Q   A   T   P   G   P   A   Y   S   G   R   E   I   -

        ATATACCCCAATGCATCCCTGCTGATCCAGAACATCATCCAGAATGACACAGGATTCTAC
    301 ---------+---------+---------+---------+---------+---------+ 360
        TATATGGGGTTACGTAGGGACGACTAGGTCTTGTAGTAGGTCTTACTGTGTCCTAAGATG

   a    I   Y   P   N   A   S   L   L   I   Q   N   I   I   Q   N   D   T   G   F   Y   -

        ACCCTACACGTCATAAAGTCAGATCTTGTGAATGAAGAAGCAACTGGCCAGTTCCGGGTA
    361 ---------+---------+---------+---------+---------+---------+ 420
        TGGGATGTGCAGTATTTCAGTCTAGAACACTTACTTCTTCGTTGACCGGTCAAGGCCCAT

   a    T   L   H   V   I   K   S   D   L   V   N   E   E   A   T   G   Q   F   R   V   -

        TACCCGGAGCTGCCCAAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAG
    421 ---------+---------+---------+---------+---------+---------+ 480
        ATGGGCCTCGACGGGTTCGGGAGGTAGAGGTCGTTGTTGAGGTTTGGGCACCTCCTGTTC

   a    Y   P   E   L   P   K   P   S   I   S   S   N   N   S   K   P   V   E   D   K   -

        GATGCTGTGGCCTTCACCTGTGAACCTGAGACTCAGGACGCAACCTACCTGTGGTGGGTA
    481 ---------+---------+---------+---------+---------+---------+ 540
        CTACGACACCGGAAGTGGACACTTGGACTCTGAGTCCTGCGTTGGATGGACACCACCCAT

   a    D   A   V   A   F   T   C   E   P   E   T   Q   D   A   T   Y   L   W   W   V   -

        AACAATCAGAGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTC
    541 ---------+---------+---------+---------+---------+---------+ 600
        TTGTTAGTCTCGGAGGGCCAGTCAGGGTCCGACGTCGACAGGTTACCGTTGTCCTGGGAG

   a    N   N   Q   S   L   P   V   S   P   R   L   Q   L   S   N   G   N   R   T   L   -

        ACTCTATTCAATGTCACAAGAAATGACACAGCAAGCTACAAATGTGAAACCCAGAACCCA
    601 ---------+---------+---------+---------+---------+---------+ 660
        TGAGATAAGTTACAGTGTTCTTTACTGTGTCGTTCGATGTTTACACTTTGGGTCTTGGGT

   a    T   L   F   N   V   T   R   N   D   T   A   S   Y   K   C   E   T   Q   N   P   -

        GTGAGTGCCAGGCGCAGTGATTCAGTCATCCTGAATGTCCTCTATGGCCCGGATGCCCCC
    661 ---------+---------+---------+---------+---------+---------+ 720
        CACTCACGGTCCGCGTCACTAAGTCAGTAGGACTTACAGGAGATACCGGGCCTACGGGGG

   a    V   S   A   R   R   S   D   S   V   I   L   N   V   L   Y   G   P   D   A   P   -
```

Figure 8

```
          ACCATTTCCCCTCTAAA      CTTACAGATCAGGGGAAAATCTGAACCTCTCCTGCC
     721  ---------+---------+---------+---------+---------+---------+  780
          TGGTAAAGGGGAGATTTGTGTAGAATGTCTAGTCCCCTTTTAGACTTGGAGAGGACGGTG

     a      T  I  S  P  L  N  T  S  Y  R  S  G  E  N  L  N  L  S  C  H   -

          GCAGCCTCTAACCCACCTGCACAGTACTCTTGGTTTGTCAATGGGACTTTCCAGCAATCC
     781  ---------+---------+---------+---------+---------+---------+  840
          CGTCGGAGATTGGGTGGACGTGTCATGAGAACCAAACAGTTACCCTGAAAGGTCGTTAGG

     a      A  A  S  N  P  P  A  Q  Y  S  W  F  V  N  G  T  F  Q  Q  S   -

          ACCCAAGAGCTCTTTATCCCCAACATCACTGTGAATAATAGTGGATCCTATACGTGCCAA
     841  ---------+---------+---------+---------+---------+---------+  900
          TGGGTTCTCGAGAAATAGGGGTTGTAGTGACACTTATTATCACCTAGGATATGCACGGTT

     a      T  Q  E  L  F  I  P  N  I  T  V  N  N  S  G  S  Y  T  C  Q   -

          GCCCATAACTCAGACACTGGCCTCAATAGGACCACAGTCACGACGATCACAGTCTATGAG
     901  ---------+---------+---------+---------+---------+---------+  960
          CGGGTATTGAGTCTGTGACCGGAGTTATCCTGGTGTCAGTGCTGCTAGTGTCAGATACTC

     a      A  H  N  S  D  T  G  L  N  R  T  T  V  T  T  I  T  V  Y  E   -

          CCACCCAAACCCTTCATCACCAGCAACAACTCCAACCCCGTGGAGGATGAGGATGCTGTA
     961  ---------+---------+---------+---------+---------+---------+ 1020
          GGTGGGTTTGGGAAGTAGTGGTCGTTGTTGAGGTTGGGGCACCTCCTACTCCTACGACAT

     a      P  P  K  P  F  I  T  S  N  N  S  N  P  V  E  D  E  D  A  V   -

          GCCTTAACCTGTGAACCTGAGATTCAGAACACAACCTACCTGTGGTGGGTAAATAATCAG
    1021  ---------+---------+---------+---------+---------+---------+ 1080
          CGGAATTGGACACTTGGACTCTAAGTCTTGTGTTGGATGGACACCACCCATTTATTAGTC

     a      A  L  T  C  E  P  E  I  Q  N  T  T  Y  L  W  W  V  N  N  Q   -

          AGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGACAACAGGACCCTCACTCTACTC
    1081  ---------+---------+---------+---------+---------+---------+ 1140
          TCGGAGGGCCAGTCAGGGTCCGACGTCGACAGGTTACTGTTGTCCTGGGAGTGAGATGAG

     a      S  L  P  V  S  P  R  L  Q  L  S  N  D  N  R  T  L  T  L  L   -

          AGTGTCACAAGGAATGATGTAGGACCCTATGAGTGTGGAATCCAGAACGAATTAAGTGTT
    1141  ---------+---------+---------+---------+---------+---------+ 1200
          TCACAGTGTTCCTTACTACATCCTGGGATACTCACACCTTAGGTCTTGCTTAATTCACAA

     a      S  V  T  R  N  D  V  G  P  Y  E  C  G  I  Q  N  E  L  S  V   -

          GACCACAGCGACCCAGTCATCCTGAATGTCCTCTATGGCCCAGACGACCCCACCATTTCC
    1201  ---------+---------+---------+---------+---------+---------+ 1260
          CTGGTGTCGCTGGGTCAGTAGGACTTACAGGAGATACCGGGTCTGCTGGGGTGGTAAAGG

     a      D  H  S  D  P  V  I  L  N  V  L  Y  G  P  D  D  P  T  I  S   -

          CCCTCATACACCTATTACCGTCCAGGGGTGAACCTCAGCCTCTCCTGCCATGCAGCCTCT
    1261  ---------+---------+---------+---------+---------+---------+ 1320
          GGGAGTATGTGGATAATGGCAGGTCCCCACTTGGAGTCGGAGAGGACGGTACGTCGGAGA

     a      P  S  Y  T  Y  Y  R  P  G  V  N  L  S  L  S  C  H  A  A  S   -

          AACCCACCTGCACAGTATTCTTGGCTGATTGATGGGAACATCCAGCAACACACACAAGAG
    1321  ---------+---------+---------+---------+---------+---------+ 1380
          TTGGGTGGACGTGTCATAAGAACCGACTAACTACCCTTGTAGGTCGTTGTGTGTGTTCTC

     a      N  P  P  A  Q  Y  S  W  L  I  D  G  N  I  Q  Q  H  T  Q  E   -

          CTCTTTATCTCCAACATCACTGAGAAGAACAGCGGACTCTATACCTGCCAGGCCAATAAC
    1381  ---------+---------+---------+---------+---------+---------+ 1440
          GAGAAATAGAGGTTGTAGTGACTCTTCTTGTCGCCTGAGATATGGACGGTCCGGTTATTG

     a      L  F  I  S  N  I  T  E  K  N  S  G  L  Y  T  C  Q  A  N  N   -
```

Figure 8, con't

```
            TCAGCCAGTGGCCACAC●   ACTACAGTCAAGACAATCACAGTCTCTGCGGAGCTGC●
     1441   ---------+---------●-------+---------+---------+-------- ●500
            AGTCGGTCACCGGTGTCGTCCTGATGTCAGTTCTGTTAGTGTCAGAGACGCCTCGACGGG

      a      S   A   S   G   H   S   R   T   T   V   K   T   I   T   V   S   A   E   L   P  -

            AAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAGGATGCTGTGGCCTTC
     1501   ---------+---------+---------+---------+---------+---------+ 1560
            TTCGGGAGGTAGAGGTCGTTGTTGAGGTTTGGGCACCTCCTGTTCCTACGACACCGGAAG

      a      K   P   S   I   S   S   N   N   S   K   P   V   E   D   K   D   A   V   A   F  -

            ACCTGTGAACCTGAGGCTCAGAACACAACCTACCTGTGGTGGGTAAATGGTCAGAGCCTC
     1561   ---------+---------+---------+---------+---------+---------+ 1620
            TGGACACTTGGACTCCGAGTCTTGTGTTGGATGGACACCACCCATTTACCAGTCTCGGAG

      a      T   C   E   P   E   A   Q   N   T   T   Y   L   W   W   V   N   G   Q   S   L  -

            CCAGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTATTCAATGTC
     1621   ---------+---------+---------+---------+---------+---------+ 1680
            GGTCAGTCAGGGTCCGACGTCGACAGGTTACCGTTGTCCTGGGAGTGAGATAAGTTACAG

      a      P   V   S   P   R   L   Q   L   S   N   G   N   R   T   L   T   L   F   N   V  -

            ACAAGAAATGACGCAAGAGCCTATGTATGTGGAATCCAGAACTCAGTGAGTGCAAACCGC
     1681   ---------+---------+---------+---------+---------+---------+ 1740
            TGTTCTTTACTGCGTTCTCGGATACATACACCTTAGGTCTTGAGTCACTCACGTTTGGCG

      a      T   R   N   D   A   R   A   Y   V   C   G   I   Q   N   S   V   S   A   N   R  -

            AGTGACCCAGTCACCCTGGATGTCCTCTATGGGCCGGACACCCCCATCATTTCCCCCCCA
     1741   ---------+---------+---------+---------+---------+---------+ 1800
            TCACTGGGTCAGTGGGACCTACAGGAGATACCCGGCCTGTGGGGGTAGTAAAGGGGGGGT

      a      S   D   P   V   T   L   D   V   L   Y   G   P   D   T   P   I   I   S   P   P  -

            GACTCGTCTTACCTTTCGGGAGCGGACCTCAACCTCTCCTGCCACTCGGCCTCTAACCCA
     1801   ---------+---------+---------+---------+---------+---------+ 1860
            CTGAGCAGAATGGAAAGCCCTCGCCTGGAGTTGGAGAGGACGGTGAGCCGGAGATTGGGT

      a      D   S   S   Y   L   S   G   A   D   L   N   L   S   C   H   S   A   S   N   P  -

            TCCCCGCAGTATTCTTGGCGTATCAATGGGATACCGCAGCAACACACACAAGTTCTCTTT
     1861   ---------+---------+---------+---------+---------+---------+ 1920
            AGGGGCGTCATAAGAACCGCATAGTTACCCTATGGCGTCGTTGTGTGTGTTCAAGAGAAA

      a      S   P   Q   Y   S   W   R   I   N   G   I   P   Q   Q   H   T   Q   V   L   F  -

            ATCGCCAAAATCACGCCAAATAATAACGGGACCTATGCCTGTTTTGTCTCTAACTTGGCT
     1921   ---------+---------+---------+---------+---------+---------+ 1980
            TAGCGGTTTTAGTGCGGTTTATTATTGCCCTGGATACGGACAAAACAGAGATTGAACCGA

      a      I   A   K   I   T   P   N   N   N   G   T   Y   A   C   F   V   S   N   L   A  -

            ACTGGCCGCAATAATTCCATAGTCAAGAGCATCACAGTCTCTGCATCTGGAACTTCTCCT
     1981   ---------+---------+---------+---------+---------+---------+ 2040
            TGACCGGCGTTATTAAGGTATCAGTTCTCGTAGTGTCAGAGACGTAGACCTTGAAGAGGA

      a      T   G   R   N   N   S   I   V   K   S   I   T   V   S   A   S   G   T   S   P  -

            GGTCTCTCAGCTGGGGCCACTGTCGGCATCATGATTGGAGTGCTGGTTGGGGTTGCTCTG
     2041   ---------+---------+---------+---------+---------+---------+ 2100
            CCAGAGAGTCGACCCCGGTGACAGCCGTAGTACTAACCTCACGACCAACCCCAACGAGAC

      a      G   L   S   A   G   A   T   V   G   I   M   I   G   V   L   V   G   V   A   L  -

            ATATAG    ←
     2101   ------ 2106
            TATATC

      a      I   *   ←
```

Figure 8, con't